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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Oct 04 13:55:14 EDT 2007

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Application No: 10584486

Version No: 1.1

Input Set:**Output Set:****Started:** 2007-10-04 13:54:26.710**Finished:** 2007-10-04 13:54:28.381**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 671 ms**Total Warnings:** 75**Total Errors:** 0**No. of SeqIDs Defined:** 85**Actual SeqID Count:** 85

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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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Input Set:

Output Set:

Started: 2007-10-04 13:54:26.710
Finished: 2007-10-04 13:54:28.381
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 671 ms
Total Warnings: 75
Total Errors: 0
No. of SeqIDs Defined: 85
Actual SeqID Count: 85

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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Finnis, Christopher J. A.

<120> Modified Plasmid and Use Thereof

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<213> *Saccharomyces cerevisiae*

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<211> 522
<212> PRT
<213> Saccharomyces cerevisiae

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Ala Val Val Lys Leu Ala Thr Asp Ser Phe Asn Glu Tyr Ile Gln Ser
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His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys
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Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu
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Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu
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Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys
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Asn Ser Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala
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370						375					380						
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Tyr	Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Arg	Leu	Ala	Pro	Thr	Tyr		
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Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile
 465 470 475 480

Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
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Asp Glu Glu Asp Ala Ile His Asp Glu Leu
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 <212> PRT
 <213> *Saccharomyces cerevisiae*

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Ala Val Val Lys Leu Ala Thr Asp Ser Phe Asn Glu Tyr Ile Gln Ser
 35 40 45

His Asp Leu Val Leu Ala Glu Phe Phe Ala Pro Trp Cys Gly His Cys
 50 55 60

Lys Asn Met Ala Pro Glu Tyr Val Lys Ala Ala Glu Thr Leu Val Glu
 65 70 75 80

Lys Asn Ile Thr Leu Ala Gln Ile Asp Cys Thr Glu Asn Gln Asp Leu
 85 90 95

Cys Met Glu His Asn Ile Pro Gly Phe Pro Ser Leu Lys Ile Phe Lys
 100 105 110

Asn Arg Asp Val Asn Asn Ser Ile Asp Tyr Glu Gly Pro Arg Thr Ala
 115 120 125

Glu Ala Ile Val Gln Phe Met Ile Lys Gln Ser Gln Pro Ala Val Ala
 130 135 140

Val Val Ala Asp Leu Pro Ala Tyr Leu Ala Asn Glu Thr Phe Val Thr
 145 150 155 160

Pro Val Ile Val Gln Ser Gly Lys Ile Asp Ala Asp Phe Asn Ala Thr
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Phe Tyr Ser Met Ala Asn Lys His Phe Asn Asp Tyr Asp Phe Val Ser	180	185	190
Ala Glu Asn Ala Asp Asp Asp Phe Lys Leu Ser Ile Tyr Leu Pro Ser	195	200	205
Ala Met Asp Glu Pro Val Val Tyr Asn Gly Lys Lys Ala Asp Ile Ala	210	215	220
Asp Ala Asp Val Phe Glu Lys Trp Leu Gln Val Glu Ala Leu Pro Tyr	225	230	235
Phe Gly Glu Ile Asp Gly Ser Val Phe Ala Gln Tyr Val Glu Ser Gly	245	250	255
Leu Pro Leu Gly Tyr Leu Phe Tyr Asn Asp Glu Glu Glu Leu Glu Glu	260	265	270
Tyr Lys Pro Leu Phe Thr Glu Leu Ala Lys Lys Asn Arg Gly Leu Met	275	280	285
Asn Phe Val Ser Ile Asp Ala Arg Lys Phe Gly Arg His Ala Gly Asn	290	295	300
Leu Asn Met Lys Glu Gln Phe Pro Leu Phe Ala Ile His Asp Met Thr	305	310	315
Glu Asp Leu Lys Tyr Gly Leu Pro Gln Leu Ser Glu Glu Ala Phe Asp	325	330	335
Glu Leu Ser Asp Lys Ile Val Leu Glu Ser Lys Ala Ile Glu Ser Leu	340	345	350
Val Lys Asp Phe Leu Lys Gly Asp Ala Ser Pro Ile Val Lys Ser Gln	355	360	365
Glu Ile Phe Glu Asn Gln Asp Ser Ser Val Phe Gln Leu Val Gly Lys	370	375	380
Asn His Asp Glu Ile Val Asn Asp Pro Lys Lys Asp Val Leu Val Leu	385	390	395
Tyr Tyr Ala Pro Trp Cys Gly His Cys Lys Arg Leu Ala Pro Thr Tyr	405	410	415
Gln Glu Leu Ala Asp Thr Tyr Ala Asn Ala Thr Ser Asp Val Leu Ile	420	425	430
Ala Lys Leu Asp His Thr Glu Asn Asp Val Arg Gly Val Val Ile Glu	435	440	445
Gly Tyr Pro Thr Ile Val Leu Tyr Pro Gly Gly Lys Lys Ser Glu Ser	450	455	460
Val Val Tyr Gln Gly Ser Arg Ser Leu Asp Ser Leu Phe Asp Phe Ile	465	470	475
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Lys Glu Asn Gly His Phe Asp Val Asp Gly Lys Ala Leu Tyr Glu Glu
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Glu Leu
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 <213> *Saccharomyces cerevisiae*

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Ile Gly Asp Ala Ala Lys Asn Gln Ala Ala Met Asn Pro Ser Asn Thr
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Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Asn Phe Asn Asp Pro Glu
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Val Gln Ala Asp Met Lys His Phe Pro Phe Lys Leu Ile Asp Val Asp
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Gly Lys Pro Gln Ile Gln Val Glu Phe Lys Gly Glu Thr Lys Asn Phe
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Thr Pro Glu Gln Ile Ser Ser Met Val Leu Gly Lys Met Lys Glu Thr
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Ala Glu Ser Tyr Leu Gly Ala Lys Val Asn Asp Ala Val Val Thr Val
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Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly
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Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Phe
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